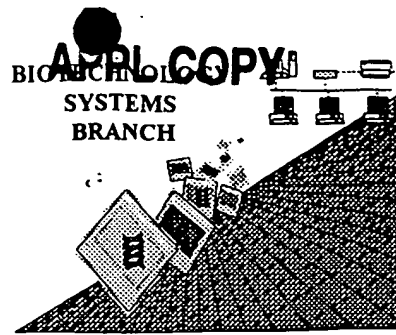




RAW SEQUENCE LISTING ERROR REPORT



16C1
#5/ K.T.
6/19
Raw
Seq.
Listing
(error)

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/721,414A
Source: OIPE
Date Processed by STIC: 5/8/2001

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

APPL COPYApplication No.: 09/221414**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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*add these
sequence
to file*

1507

1517

W-->

W--> 26 <221> NAME/KEY: n represents a, t, g or c

W-->

pg 1-3

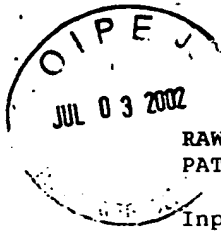
Does Not Comply
Corrected Diskette Needed

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this goes on a <223> line (per 1.823 of sequence rules)

*(create a new
<223> line)*

3 <110> APPLICANT: Suga, Hiroaki
5 <120> TITLE OF INVENTION: Catalytic RNA Molecules with Aminoacylation Activity
7 <130> FILE REFERENCE: 11520.0222
10 <140> CURRENT APPLICATION NUMBER: US 09/721,414A
11 <141> CURRENT FILING DATE: 2000-11-22
13 <150> PRIOR APPLICATION NUMBER: US 60/167,331
14 US 60/214,382 → *<150> US 60/214,382*
15 <151> PRIOR FILING DATE: 1999-11-24
16 2000-06-28 → *<151> 2000-06-28*
18 <160> NUMBER OF SEQ ID NOS: 22
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 110
22 <212> TYPE: DNA
23 <213> ORGANISM: artificial sequence
25 <220> FEATURE:
26 <221> NAME/KEY: n represents a, t, g or c
27 <222> LOCATION: 21-90
28 <223> OTHER INFORMATION: synthetic oligonucleotide containing random pool of 70
29 nucleotides
31 <400> SEQUENCE: 1
33 ggatcgctcag tgcattgaga nnnnnnnnnn nnnnnnnnnn 40
34 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 80
35 nnnnnnnnnn ggtggtatcc ccaaggggta 110
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 76
39 <212> TYPE: DNA
40 <213> ORGANISM: artificial sequence
42 <220> FEATURE:
43 <223> OTHER INFORMATION: completely synthesized primer complementary to the oRNAgln
45 <400> SEQUENCE: 2
46 tggtcgcggt acgaggattc gaacctcgga atgccggatt 40
47 tagaaatccg gtcccttacc ccttggggat accacc 76
50 <210> SEQ ID NO: 3
51 <211> LENGTH: 52
52 <212> TYPE: DNA
53 <213> ORGANISM: artificial sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: 5' primer containing T7 promoter sequence
58 <400> SEQUENCE: 3
59 ggtaacacgc atatgtaata cgactcacta taggatcgtc 40
60 agtgcattga ga 52
62 <210> SEQ ID NO: 4
63 <211> LENGTH: 20
64 <212> TYPE: DNA
65 <213> ORGANISM: artificial sequence
67 <220> FEATURE:
68 <223> OTHER INFORMATION: 3' completely synthesized primer



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70 <400> SEQUENCE: 4
71 tggctgcggt acgaggattc 20
73 <210> SEQ ID NO: 5
74 <211> LENGTH: 146
75 <212> TYPE: RNA
76 <213> ORGANISM: artificial sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: pre-12 catalytic RNA
81 <400> SEQUENCE: 5
82 ggaucgucag ugcauugaga uuuccgcagc ccuucucacu 40
83 aacggugggu cauggguauu ggcguuaggu gcgggaugcu 80
84 acgcuggugg uauccccaag gguacgggac cggacaauucg 120
85 agauucgaau ccucguaccg cagcca 146
88 <210> SEQ ID NO: 6
89 <211> LENGTH: 151
90 <212> TYPE: RNA
91 <213> ORGANISM: artificial sequence
93 <220> FEATURE:
W--> 94 <221> NAME/KEY: n represents a, g or c
95 <222> LOCATION: 12
96 <223> OTHER INFORMATION: pre-38 catalytic RNA
98 <400> SEQUENCE: 6
OK 99 ggaucgucag uncauugaga uuuccgcagc ccuucucacu 40
100 aacggugggu ucauggguau uggcguuagg ugcgggaugc 80
101 uacuacgcug gugguauccc caaggguaacg ggaccggaucc 120
102 auucgagauu cgaauccucg uaccgcagcc a 151
105 <210> SEQ ID NO: 7
106 <211> LENGTH: 150
107 <212> TYPE: RNA
108 <213> ORGANISM: artificial sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: pre-29 catalytic RNA
114 <400> SEQUENCE: 7
115 ggaucgucag ugcauugaga uuuccgcagg cccuucucac 40
116 uaacggugggu ucauggguau uggcguuagg ugcgggaugc 80
117 uacuacgcug gugguauccc caaggguaacg ggaccggaca 120
118 uucgagauuc gaaucucug accgcagcca 150
120 <210> SEQ ID NO: 8
121 <211> LENGTH: 150
122 <212> TYPE: RNA
123 <213> ORGANISM: artificial sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: pre-36 catalytic RNA
128 <400> SEQUENCE: 8
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130 aacggugggu cauggguauu ggcguuaggu gcgggaugcu 80
131 acuacgcugg ugguaucccc aaggguaacg gaccggauca 120
132 uucgagauuc gaaucucug accgcagcca 150
134 <210> SEQ ID NO: 9

*is not permitted in an RNA sequence - use "n" instead
more exploration to (223)*

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135 <211> LENGTH: 150
 136 <212> TYPE: RNA
 137 <213> ORGANISM: artificial sequence
 139 <220> FEATURE:
 140 <223> OTHER INFORMATION: pre-24 catalytic RNA
 142 <400> SEQUENCE: 9
 143 ggaucgucag ugcauugaga uuuccgcagg ccuucucac 40
 144 uaacgguggg ucauggguau ugccguuagg ugcgggaugc 80
 145 uacuacgcug gugguauccc caaggguacg ggaccggaca 120
 146 uucgagauuc gaauccucgu accgcagcca 150

148 <210> SEQ ID NO: 10
 149 <211> LENGTH: 149
 150 <212> TYPE: RNA
 151 <213> ORGANISM: artificial Sequence
 153 <220> FEATURE:
 154 <223> OTHER INFORMATION: pre-25 catalytic RNA
 156 <400> SEQUENCE: 10
 157 ggaucgucag ugcauugaga uuuccgcagc ccuucucacu 40
 158 aacggugggu cauggguauu ggcguuaggu gcgggaugcu 80
 159 acuacgcugg ugguaucccc aaggguacg gaccggacau 120
 160 ucgagauucg aauccucgua ccgcagcca 149

163 <210> SEQ ID NO: 11
 164 <211> LENGTH: 149
 165 <212> TYPE: RNA
 166 <213> ORGANISM: artificial Sequence
 168 <220> FEATURE:
 169 <223> OTHER INFORMATION: pre-22 catalytic RNA
 171 <400> SEQUENCE: 11
 172 ggaucgucag ugcauugaga uuuccgcagc ccuucucacu 40
 173 aacggugggu cauggguguu ggcguuaggu gcgggaugcu 80
 174 acuacgcugg ugguaucccc aaggguacg gaucggacau 120
 175 ucgagauucg aauccucgua ccgcagcca 149

178 <210> SEQ ID NO: 12
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 180 <212> TYPE: RNA

181 <213> ORGANISM: artificial Sequence

183 <220> FEATURE:

W--> 184 <221> NAME/KEY: n represents a ^ug, g or c

185 <222> LOCATION: 112

186 <223> OTHER INFORMATION: pre-5 catalytic RNA

188 <400> SEQUENCE: 12

189 ggaucgucag ugcauugaga uuuccgcagc ccuucucacu 40

190 aacggugggu cauggguauu ggcguuaggu gcgggaugcu 80

OK-> 191 acuacgcugg ugguaucccc aaggguacg gnccggacau 120

192 ucgagauucg aauccucgua ccgcagcca 149

195 <210> SEQ ID NO: 13

196 <211> LENGTH: 149

197 <212> TYPE: RNA

198 <213> ORGANISM: artificial Sequence

← move explanation to <223>

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Input Set : A:\corrected sequence listing US non-prov. Suga.txt

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200 <220> FEATURE:
201 <223> OTHER INFORMATION: pre-19 catalytic RNA
203 <400> SEQUENCE: 13
204 ggaucgucag ugcauugaga uuuccgcagc ccuucucacu      40
205 aacggguaggu cauggguauu ggcguuaggu gcgggaugcu      80
206 acuacgcugg ugguauccccc aaggguacgg gaccggacau     120
207 ucgagauucg aaucucgua ccgcagcca                     149
210 <210> SEQ ID NO: 14
211 <211> LENGTH: 150
212 <212> TYPE: RNA
213 <213> ORGANISM: artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: pre-8 catalytic RNA
218 <400> SEQUENCE: 14
219 ggaucgucag ugcauugaga uuuccgcagc ccuucucacu      40
220 aacggugggg ucauggguau ugcguuagg ugcgggaugc      80
221 uacuacgcug gugguauccu caaggguaacg ggaccggaca     120
222 uucuagauuc gaaucucgu accgcagcca                     150
225 <210> SEQ ID NO: 15
226 <211> LENGTH: 148
227 <212> TYPE: RNA
228 <213> ORGANISM: artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: pre-23 catalytic RNA
233 <400> SEQUENCE: 15
234 ggaucgucag ugcauugaga uuuccgcagc ccuucucacu      40
235 aacggugggg cauggguauu ggcguuaggu gcgggaugcu      80
236 acuacgcugg ugguauccccc aggguaacgg accggacau     120
237 cgagauucga auccucguac cgacagcca                     148
240 <210> SEQ ID NO: 16
241 <211> LENGTH: 75
242 <212> TYPE: RNA
243 <213> ORGANISM: Escherichia coli
245 <220> FEATURE:
246 <223> OTHER INFORMATION: otRNA
248 <400> SEQUENCE: 16
249 ggugguaucc ccaaggggua agggaccgga uucuaaaucc      40
250 ggcauuccga gguucgaauc cucguaccgc agcca             75
252 <210> SEQ ID NO: 17
253 <211> LENGTH: 160
254 <212> TYPE: RNA
255 <213> ORGANISM: artificial sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: H2 Leu catalytic RNA
260 <400> SEQUENCE: 17
261 ggaucgucag ugcauugaga ugcccaaagc ccuucucacu      40
262 uccggugggg caugcguuau ugcguuaggu gaggaugcu      80
263 aguaugcggg ugguauccaa gggguaaggg accggauucu     120
264 aaauccgcau uccgagguuc gaaucucgu accgcagcca         160

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Input Set : A:\corrected sequence listing US non-prov. Suga.txt

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266 <210> SEQ ID NO: 18
267 <211> LENGTH: 156
268 <212> TYPE: RNA
269 <213> ORGANISM: artificial sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: D1-Leu catalytic RNA
274 <400> SEQUENCE: 18
275 ggauCGuacag ugcauGaga uagugacacU aggcgggggg      40
276 ugauagcgca uuugagguu ugguuugggg gguuauGcgU      80
277 gaguucuugg gugguaucCa agggguaagg gaucuaaauc      120
278 cgacauuccg agguucgaau ccucguaccg cagcca      156
281 <210> SEQ ID NO: 19
282 <211> LENGTH: 35
283 <212> TYPE: RNA
284 <213> ORGANISM: artificial sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: RNA forming a minihelix
289 <400> SEQUENCE: 19
290 ggugguacga gguucgaauC cucguaccgc agcca      35
292 <210> SEQ ID NO: 20
293 <211> LENGTH: 73
294 <212> TYPE: RNA
295 <213> ORGANISM: artificial sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: V1 variant of tRNA
300 <400> SEQUENCE: 20
301 ggugguaucC ccaaggguaC gggaccggau ucuaaaucCg      40
302 gcauucgaga uucgaauccU cguaccgcag cca      73
304 <210> SEQ ID NO: 21
305 <211> LENGTH: 75
306 <212> TYPE: RNA
307 <213> ORGANISM: artificial sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: V2 variant of tRNA
312 <400> SEQUENCE: 21
313 ggugguaucC ccaaggggua cgggaccgga uucuaaaucC      40
314 ggcauuccga gauucgaauC cucguaccgc agcca      75
317 <210> SEQ ID NO: 22
318 <211> LENGTH: 73
319 <212> TYPE: RNA
320 <213> ORGANISM: artificial sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: V3 variant of tRNA
325 <400> SEQUENCE: 22
327 ggugguaucC ccaaggguaa gggaccggau ucuaaaucCg      40
328 gcauucgagg uucgaauccU cguaccgcag cca      73

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VERIFICATION SUMMARY

DATE: 05/08/2001

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Input Set : A:\corrected sequence listing US non-prov. Suga.txt

Output Set: N:\CRF3\05082001\I721414A.raw

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L:16 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:
L:26 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:94 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:99 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:184 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12